OLD 27 7005 W

SEQUENCE LISTING

0> Johnson, Leslie S.

Li, Hua

Tuaillon, Nadine

<120> SOLUBLE FCgammaR FUSION PROTEINS AND METHODS OF USE THEREOF

<130> 11183-005-999

<140> 10/756,153

<141> 2004-01-13

<150> 60/439,709

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<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIa-G2

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Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
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Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser 35 40 45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val 50 55 60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser 65 70 75 80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Gln Ala 85 90 95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His

100 105 110

Ser Trp	Lys 115	Asn	Thr	Ala	Leu	His 120	Lys	Val	Thr	Tyr	Leu 125	Gln	Asn	Gly
Lys Gly		Lys	Tyr	Phe	His 135	His	Asn	Ser	Asp	Phe 140	Tyr	Ile	Pro	Lys
Ala Thr 145	Leu	Lys	Asp	Ser 150	Gly	Ser	Tyr	Phe	Cys 155	Arg	Gly	Leu	Val	Gly 160
Ser Lys	Asn	Val	Ser 165	Ser	Glu	Thr	Val	Asn 170	Ile	Thr	Ile	Thr	Gln 175	Gly
Leu Ala	Val	Ser 180	Thr	Ile	Ser	Ser	Phe 185	Phe	Pro	Pro	Gly	Tyr 190	Gln	Val
Glu Arg	Lys 195	Cys	Cys	Val	Glu	Cys 200	Pro	Pro	Cys	Pro	Ala 205	Pro	Pro	Val
Ala Gly 210		Ser	Val	Phe	Leu 215	Phe	Pro	Pro	Lys	Pro 220	Lys	Asp	Thr	Leu
Met Ile 225	e Ser	Arg	Thr	Pro 230	Glu	Val	Thr	Cys	Val 235	Val	Val	Asp	Val	Ser 240
His Glu	ı Asp	Pro	Glu 245	Val	Gln	Phe	Asn	Trp 250	Tyr	Val	Asp	Gly	Met 255	Glu
Val His	. Asn	Ala 260	Lys	Thr	Lys	Pro	Arg 265	Glu	Glu	Gln	Phe	Asn 270	Ser	Thr
Phe Arg	Val 275	Val	Ser	Val	Leu	Thr 280	Val	Val	His	Gln	Asp 285	Trp	Leu	Asn
Gly Lys		Tyr	Lys	Cys	Lys 295	Val	Ser	Asn	Lys	Gly 300	Leu	Pro	Ala	Pro
Ile Glu 305	Lys	Thr	Ile	Ser 310	Lys	Thr	Lys	Gly	Gln 315	Pro	Arg	Glu	Pro	Gln 320
Val Tyı	Thr	Leu	Pro 325	Pro	Ser	Arg		Glu 330		Thr	Lys	Asn	Gln 335	
Ser Le	Thr	Cys 340	Leu	Val	Lys	Gly	Phe 345	Tyr	Pro	Ser	Asp	Ile 350	Ala	Val
Glu Tr	355	Ser	Asn	Gly	Gln	Pro 360	Glu	Asn	Asn	Tyr	Lys 365	Thr	Thr	Pro
Pro Met		Asp	Ser	Asp	Gly 375	Ser	Phe	Phe	Leu	Tyr 380	Ser	Lys	Leu	Thr
Val Asp 385	Lys	Ser	Arg	Trp 390	Gln	Gln	Gly	Asn	Val 395	Phe	Ser	Cys	Ser	Val 400
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<223> sFcRIIb-G2

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Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr 20 25 30

His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu 35 40 45

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn 50 55 60

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp 70 75 80

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro 85 90 95

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser 100 105 110

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys
115 120 125

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala 130 135 140

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr 145 150 155 160

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser 165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys 180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 210 215 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr 225 230 235 240 Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 245 250 250 255

260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 275 280 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln 290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 340 345 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val 370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

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<223> sFcRIIa(131R)-G2

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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro 20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly 50 55 60

Glu 1 65	Tyr	Thr	Cys	Gln	Thr 70	Gly	Gln	Thr	Ser	Leu 75	Ser	Asp	Pro	Val	His 80
Leu T	Thr	Val	Leu	Ser 85	Glu	Trp	Leu	Val	Leu 90	Gln	Thr	Pro	His	Leu 95	Glu
Phe C	Gln	Glu	Gly 100	Glu	Thr	Ile	Met	Leu 105	Arg	Cys	His	Ser	Trp 110	Lys	Asp
Lys E	Pro	Leu 115	Val	Lys	Val	Thr	Phe 120	Phe	Gln	Asn	Gly	Lys 125	Ser	Gln	Lys
Phe S	Ser 130	Arg	Leu	Asp	Pro	Thr 135	Phe	Ser	Ile	Pro	Gln 140	Ala	Asn	His	Ser
His S 145	Ser	Gly	Asp	Tyr	His 150	Cys	Thr	Gly	Asn	Ile 155	Gly	Tyr	Thr	Leu	Phe 160
Ser S	Ser	Lys	Pro	Val 165	Thr	Ile	Thr	Val	Gln 170	Val	Pro	Ser	Met	Gly 175	Ser
Ser S	Ser	Pro	Met 180	Glu	Glu	Arg	Lys	Cys 185	Cys	Val	Glu	Cys	Pro 190	Pro	Cys
Pro A	Ala	Pro 195	Pro	Val	Ala	Gly	Pro 200	Ser	Val	Phe	Leu	Phe 205	Pro	Pro	Lys
Pro I	Lys 210	Asp	Thr	Leu	Met	Ile 215	Ser	Arg	Thr	Pro	Glu 220	Val	Thr	Cys	Val
Val V 225	Val	Asp	Val	Ser	His 230	Glu	Asp	Pro	Glu	Val 235	Gln	Phe	Asn	Trp	Tyr 240
Val A	Asp	Gly	Met	Glu 245	Val	His	Asn	Ala	Lys 250	Thr	Lys	Pro	Arg	Glu 255	Glu
Gln F	Phe	Asn	Ser 260	Thr	Phe	Arg	Val	Val 265	Ser	Val	Leu	Thr	Val 270	Val	His
Gln A	Asp	Trp 275	Leu	Asn	Gly	Lys	Glu 280	Tyr	Lys	Cys	Lys	Val 285	Ser	Asn	Lys
Gly I	Leu 290	Pro	Ala	Pro	Ile	Glu 295	Lys	Thr	Ile	Ser	Lys 300	Thr	Lys	Gly	Gln
Pro <i>P</i> 305	Arg	Glu	Pro	Gln	Val 310	Tyr	Thr	Leu	Pro	Pro 315	Ser	Arg	Glu	Glu	Met 320
Thr I	Lys	Asn	Gln	Val 325	Ser	Leu	Thr	Cys	Leu 330	Val	Lys	Gly	Phe	Tyr 335	Pro
Ser A	Asp	Ile	Ala 340	Val	Glu	Trp	Glu	Ser 345	Asn	Gly	Gln	Pro	Glu 350	Asn	Asn
Tyr I	Lys	Thr 355	Thr	Pro	Pro	Met	Leu 360	Asp	Ser	Asp	Gly	Ser 365	Phe	Phe	Leu
Tyr S	Ser 370	Lys	Leu	Thr	Val	Asp 375	Lys	Ser	Arg	Trp	Gln 380	Gln	Gly	Asn	Val
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Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

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To de la constitución de la cons

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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
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Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr 35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly 50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His 65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu 85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp 100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys 115 120 125

Phe Ser His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser 130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe 145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser 165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys 180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys

195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

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Gly	Leu 290	Pro	Ala	Pro	Ile	Glu 295	Lys	Thr	Ile	Ser	Lys 300	Thr	Lys	Gly	Gln	
Pro 305	Arg	Glu	Pro	Gln	Val 310	Tyr	Thr	Leu	Pro	Pro 315	Ser	Arg	Glu	Glu	Met 320	
Thr	Lys	Asn	Gln	Val 325	Ser	Leu	Thr	Cys	Leu 330	Val	Lys	Gly	Phe	Tyr 335	Pro	
Ser	Asp	Ile	Ala 340	Val	Glu	Trp	Glu	Ser 345	Asn	Gly	Gln	Pro	Glu 350	Asn	Asn	
Tyr	Lys	Thr 355	Thr	Pro	Pro	Met	Leu 360	Asp	Ser	Asp	Gly	Ser 365	Phe	Phe	Leu	
Tyr	Ser 370	Lys	Leu	Thr	Val	Asp 375	Lys	Ser	Arg	Trp	Gln 380	Gln	Gly	Asn	Val	
Phe 385	Ser	Cys	Ser	Val	Met 390	His	Glu	Ala	Leu	His 395	Asn	His	Tyr	Thr	Gln 400	
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Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys Phe Ser

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- Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
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- Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
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- Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
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- Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
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- Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn 225 230 235 240
- Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile

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Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Gln Ala 85 90 95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His 100 105 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly 115 120 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys 130 135 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly 145 150 155 160

Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln Gly 165 170 175

Gly Gly Gly Ser Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro 180 185 190

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro 195 200 205

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val 210 215 220

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val 225 230 235 240

Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Glu 245 250 255

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln 260 265 270

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly 275 280 285

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro 290 295 300

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr 305 310 315 320

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser 325 330 335

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr 340 345 350

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 355 360 365

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe 370 375 380

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys 385 390 395 400

Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 35

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

<400> 35 atgcqqactq aaqatctccc caaqqctqtq qtqttcctqq agcctcaatq qtacagggtq 60 ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120 acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180 gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc cacctcagt 240 qacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300 ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360 aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420 tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480 agtaaaaatg tgtcttcaga gactgtgacc atcaccatca ctcaaggtgg cggaggatca 540 gagegeaaat gttgtgtega gtgeecaceg tgeecageac cacetgtgge aggaeegtea 600 qtcttcctct tcccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 660 acqtqcqtqq tqqtqqacqt qaqccacqaa gaccccgagg tccagttcaa ctggtacgtg 720 gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 780 ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac 840 aagtgcaagg totocaacaa aggcotocca goooccatog agaaaaccat otocaaaacc 900 aaaqqqcaqc cccqaqaacc acaqqtqtac accctqcccc catcccqqqa qqaqatgacc 960 aaqaaccaqq tcaqcctqac ctqcctqqtc aaaqqcttct accccaqcqa catcqccqtg 1020 gaqtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 1080 tecgaegget cettetteet etacageaag etcaeegtgg acaagageag gtggeageag 1140 gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1200 agcctctccc tgtctccggg taaa 1224

<210> 36

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

Trp	Tyr	Arg	Val 20	Ļeu	Glu	Lys	Asp	Ser 25	Val	Thr	Leu	Lys	Cys 30	Gln	Gly
Ala	Tyr	Ser 35	Pro	Glu	Asp	Asn	Ser 40	Thr	Gln	Trp	Phe	His 45	Asn	Glu	Ser
Leu	Ile 50	Ser	Ser	Gln	Ala	Ser 55	Ser	Tyr	Phe	Ile	Asp 60	Ala	Ala	Thr	Val
Asp 65	Asp	Ser	Gly	Glu	Tyr 70	Arg	Cys	Gln	Thr	Asn 75	Leu	Ser	Thr	Leu	Ser 80
Asp	Pro	Val	Gln	Leu 85	Glu	Val	His	Ile	Gly 90	Trp	Leu	Leu	Leu	Gln 95	Ala
Pro	Arg	Trp	Val 100	Phe	Lys	Glu	Glu	Asp 105	Pro	Ile	His	Leu	Arg 110	Cys	His
Ser	Trp	Lys 115	Asn	Thr	Ala	Leu	His 120	Lys	Val	Thr	Tyr	Leu 125	Gln	Asn	Gly
Lys	Gly 130	Arg	Lys	Tyr	Phe	His 135	His	Asn	Ser	Asp	Phe 140	Tyr	Ile	Pro	Lys
Ala 145	Thr	Leu	Lys	Asp	Ser 150	Gly	Ser	Tyr	Phe	Cys 155	Arg	Gly	Leu	Val	Gly 160
Ser	Lys	Asn	Val	Ser 165	Ser	Glu	Thr	Val	Thr 170	Ile	Thr	Ile	Thr	Gln 175	Gly
Gly	Gly	Gly	Ser 180	Glu	Arg	Lys	Cys	Cys 185	Val	Glu	Cys	Pro	Pro 190	Cys	Pro
Ala	Pro	Pro 195	Val	Ala	Gly	Pro	Ser 200	Val	Phe	Leu	Phe	Pro 205	Pro	Lys	Pro
Lys	Asp 210	Thr	Leu	Met	Ile	Ser 215	Arg	Thr	Pro	Glu	Val 220	Thr	Cys	Val	Val
Val 225	Asp	Val	Ser	His	Glu 230	Asp	Pro	Glu	Val	Gln 235	Phe	Asn	Trp	Tyr	Val 240
Asp	Gly	Met	Glu	Val 245	His	Asn	Ala	Lys	Thr 250	Lys	Pro	Arg	Glu	Glu 255	Gln
Phe	Asn	Ser	Thr 260	Phe	Arg	Val	Val	Ser 265	Val	Leu	Thr	Val	Val 270	His	Gln
Asp	Trp	Leu 275	Asn	Gly	Lys	Glu	Tyr 280	Lys	Cys	Lys	Val	Ser 285	Asn	Lys	Gly
Leu	Pro 290	Ala	Pro	Ile	Glu	Lys 295	Thr	Ile	Ser	Lys	Thr 300	Lys	Gly	Gln	Pro
Arg 305	Glu	Pro	Gln	Val	Tyr 310	Thr	Leu	Pro	Pro	Ser 315	Arg	Glu	Glu	Met	Thr 320
Lys	Asn	Gln	Val	Ser 325	Leu	Thr	Cys	Leu	Val 330	Lys	Gly	Phe	Tyr	Pro 335	Ser

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr 340 345 350

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr 355 360 365

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe 370 375 380

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys 385 390 395 400

Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 37

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 37 atgcqqactg aagatctccc caaggctgtg gtgttcctgg agcctcaatg gtacagggtg 60 ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120 acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180 qctqccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240 gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300 ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360 aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420 tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480 agtaaaaatg tgtcttcaga gactgtgaac atcactgtcc aagctcccag ctcttcaccc 540 atggaggagc gcaaatgttg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 600 ccqtcaqtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 660 gaggtcacgt gcgtggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 720 tacgtggacg gcatggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 780 agcacgttcc gtgtggtcag cgtcctcacc gtcgtgcacc aggactggct gaacggcaag 840 gagtacaagt gcaaggtctc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc 900 aaaaccaaag ggcagcccg agaaccacag gtgtacaccc tgccccatc ccgggaggag 960
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1020
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1080
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1140
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1200
cagaagagcc tctccctgtc tccgggtaaa 1230

<210> 38

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 38

Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln
1 10 15

Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly 20 25 30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser 35 40 45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val 50 55 60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser 65 70 75 80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Gln Ala 85 90 95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His 100 105 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly 115 120 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys 130 135 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly 145 150 155 160

Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Val Gln Ala Pro 165 170 175 Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 215 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 250 Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 330 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe 355 360 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 395 385 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 39

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V4

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<400> 39
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ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120
acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180
gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240
gacceggtge agetagaagt ceatategge tggetgttge teeaggeece teggtgggtg 300
ttcaaggagg aagaccetat teacetgagg tgteacaget ggaagaacae tgetetgeat 360
aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420
tacattccaa aagccacact caaagacage ggctcctact tetgcagggg gettgttggg 480
agtaaaaatg tgtcttcaga gactgtgacc atcactgtcc aagctcccag ctcttcaccc 540
atggaggage gcaaatgttg tgtcgagtge ceaecgtgee cageaceaec tgtggeagga 600
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 660
gaggtcacgt gcgtggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 720
tacgtggacg gcatggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 780
agcacgttcc gtgtggtcag cgtcctcacc gtcgtgcacc aggactggct gaacggcaag 840
gagtacaagt gcaaggtete caacaaagge eteceageee ecategagaa aaceatetee 900
aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 960
atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1020
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1080
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1140
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1200
cagaagagcc tctccctgtc tccgggtaaa
                                                                  1230
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<210> 40
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<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V4

<400> 40 Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly 115 Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys 135 Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly 155 Ser Lys Asn Val Ser Ser Glu Thr Val Thr Ile Thr Val Gln Ala Pro 170 Ser Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro 185 Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys 220 210 215 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp 230 235 Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu 250 245 Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val 265 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn 280 285 Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu 315

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr 325 330 335

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn 340 345 350

Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe 355 360 365

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn 370 375 380

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr 385 390 395 400

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 405 410

<210> 41

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIBG2-N297Q

<400> 41
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caggaggact ctgtgactct gacatgccgg gggactcaca gccctgagag cgactccatt 120
cagtggttcc acaatgggaa tctcattccc acccacacgc agcccagcta caggttcaag 180
gccaacaaca atgacagcgg ggagtacacg tgccagactg gccagaccag cctcagcgac 240
cctgtgcatc tgactgtgct ttctgagtgg ctggtgctcc agacccctca cctggagttc 300
caggagggag aaaccatcgt gctgaggtgc cacagctgga aggacaagcc tctggtcaag 360
gtcacattct tccagaatgg aaaatccaag aaattttccc gttcggatcc caacttctcc 420
atcccacaag caaaccacag tcacagtggt gattaccact gcacaggaaa cataggctac 480
acgctgttct catccaagcc tgtgaccatc actgtccaag ctcccagctc ttcacccatg 540
gaggagcgca aatgttgtg cgagtgcca ccgtgcccag caccacctgt ggcaggaccg 600
tcagtcttcc tctccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 660
gtcacgtgcg tggtggtga cgtgagccac gaagaccccg aggtccagtt caactggtac 720
gtggacggca tggaggtgca taatgccaag acaaagccac gggaggagca gttccagaga 840
acgtttccgtg tggtcagcg cctcaccgtc gtgcaccagg actggctgaa cggcaaggag 840

tacaagtgca aggtctcaa caaaggcctc ccagcccca tcgagaaaac catctccaaa 900 accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 960 accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctacccaag cgacatcgcc 1020 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1080 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1140 caggggaacg tcttctacatg ctctgtgatg catgaggctc tgcacaacca ctacacaca 1200 aagagcctct ccctgtctcc gggtaaa

<210> 42

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIBG2-N297Q

<400> 42

Thr Pro Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp
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Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr 20 25 30

His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu 35 40 45

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn 50 55 60

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp 65 70 . 75 80

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro 85 90 95

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser 100 105 110

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys
115 120 125

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala 130 135 140

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr 145 150 155 160 Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser 165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys 180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val 210 215 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr 225 230 235 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu 245 250 255

Gln Phe Gln Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His 260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys 275 280 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln 290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met 305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro 325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn 340 345 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu 355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val 370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln 385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys 405

<210> 43

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaRIIIA F/G loop region fragment

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<400> 43
Gly Ser Lys Asn Val
<210> 44
<211> 5
<212> PRT
<213> Artificial Sequence
<220>
<223> FcgammaRIIIA F/G loop region mutant
<400> 44
Gly Tyr Thr Leu Phe
<210> 45
<211> 16
<212> PRT
<213> Homo sapiens
<220>
<223> FcgammaRIIIA-G2 extracellular domain C-terminal fragment
<400> 45
Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln Val
                                                         15
                 5
<210> 46
<211> 5
<212> PRT
<213> Artificial Sequence
<220>
<223> flexible linker sequence
<400> 46
Gly Gly Gly Ser
<210> 47
<211> 20
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<212> PRT
<213> Homo sapiens
<220>
<223> FcgammaRIIIA-G2 extracellular domain C-terminal fragment
<400> 47
Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro
                                     10
Gly Tyr Gln Val
            20
<210> 48
<211> 10
<212> PRT
<213> Homo sapiens
<220>
<223> FcgammaRIIB-G2 extracellular domain C-terminal fragment
Val Gln Ala Pro Ser Ser Ser Pro Met Glu
                 5
<210> 49
<211> 24
<212> PRT
<213> Homo sapiens
<220>
<223> FcgammaRIIIA-G2 wild type subsequence
<400> 49
Val Asn Ile Thr Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser
Phe Phe Pro Pro Gly Tyr Gln Val
            20
<210> 50
<211> 12
<212> PRT
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<213> Artificial Sequence

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<220>
<223> FcgammaRIIIA-G2, V1 subsequence
<400> 50
Val Asn Ile Thr Ile Thr Gln Gly Gly Gly Ser
<210> 51
<211> 12
<212> PRT
<213> Artificial Sequence
<220>
<223> FcgammaRIIIA-G2, V2 subsequence
<400> 51
Val Thr Ile Thr Ile Thr Gln Gly Gly Gly Ser
<210> 52
<211> 14
<212> PRT
<213> Artificial Sequence
<220>
<223> FcgammaRIIIA-G2, V3 subsequence
<400> 52
Val Asn Ile Thr Val Gln Ala Pro Ser Ser Pro Met Glu
                                    10
<210> 53
<211> 14
<212> PRT
<213> Artificial Sequence
<220>
<223> FcgammaRIIIA-G2, V4 subsequence
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<400> 53

Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Glu 1 5 10

<210> 54

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<223> FcgammaRIIB-G2 wild type subsequence

<400> 54

Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Glu 1 5 10